

**In the Drawings:**

Please replace the drawings of Figures 1A-E (5 sheet) with the corrected drawings of Figures 1A-E submitted herewith (5 sheets).

Please replace the drawings of Figures 25D-I (3 sheets) with the corrected drawings of Figures 25D-I submitted herewith (3 sheets).

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GTCCCTTCCACCATGCCACTCGCTGGGCTTCTTCTCTGTGGCGTGTCTCTCTGCTCGCGCGCTG  
1 60  
CAGGAAGGTGGTACGTGAGCGACCCGAAAGAGACACCGCACAAAGAGACGAGCGCGGAC  
M H S L G F F S V A C S L L A A A -  
CGCTGCTCCCGGTCCTCGGAGGCGCCCGCGCGCGCGCTTTCGAGTCCGGACTCG  
120  
GCGACGAGGGCCAGGAGCGCTCCGGGGCGGGCGGGCGGGAAGCTCAGGCCTGAGC  
61  
L L P G P R E A P A A A A A F E S G L D -  
ACCTCTCGGACGCGAGCCCGACGCGGGCGAGGCCACGGCTTATGCAAGCAAAGATCTGG  
180  
TGGAGAGCCTGCGCCTCGGGCTCGGCGCCCGCTCCGGTGCCGAATACGTTCTTCTAGACC  
L S D A E P D A G E A T A Y A S K D L E -  
AGGAGCAGTTACGGTCTGTGTCCAGGTGATGAAGTCACTGACTGTACTCTACCCAGAAT  
181 240  
TCCTCGTCAATGCCAGACACAGGTCACATCTACTGAGTACTGACATGAGATGGGTCTTA  
E Q L R S V S S V D E L M T V L Y P E Y -  
ATTGGAAAATGTACAAGTGTGAGCTAAGGAAAGGAGGCTGGCAACATAACAGAGAACAGG  
300  
TAACCTTTTACATGTTACAGTCGATTCCCTTCCCGACCGTTGTATTGTCTCTTGTCC  
241  
W K M Y K C Q L R K G G W Q H N R E Q A -  
CCAACCTCAACTCAAGGACAGAGAGACTATAAAATTGCTGCAGCACATTATAATACAG

**FIG. 1A**



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661 TTTACAGACAAGTTCCATTATTAGACGTTCCCTGCCAGCAACACTACCACAGTGTC 720  
-----+-----+-----+-----+-----+-----+  
AAATGTCTGTTCAAGTAAGGTAATAATCTGCAAGGACGGTCGTTGTGATGGTGTACACAG  
Y R Q V H S I I R R S L P A T L P Q C Q -  
721 AGGCAGCGAACAAGACCTGCCCCACCAATTACATGTGGAATAATCACAATCTGCAGATGCC 780  
-----+-----+-----+-----+-----+-----+  
TCCGTCGCTTGTCTGACGGGGTGGTTAATGTACACCTTATTAGTGTAGACGCTCTACGG  
A A N K T C P T N Y M W N N H I C R C L -  
781 TGGCTCAGGAAGATTATGTTTTCTCCTCGGATGCTGGAGATGACTCAACAGATGGATTCC 840  
-----+-----+-----+-----+-----+-----+  
ACCGAGTCCTTCTAAATAACAAAGGAGCCTACGACCTCTACTGAGTTGTCTACCTAAGG  
A Q E D F M F S S D A G D D S T D G F H -  
841 ATGACATCTGTGGACCAACAAGGAGCTGGATGAAGAGACCTGTCAGTGTCTGCAGAG 900  
-----+-----+-----+-----+-----+-----+  
TACTGTAGACACCTGGTTGTTCTCCGACCTACTTCTCTGGACAGTCAACACAGACGTCTC  
D I C G P N K E L D E E T C Q C V C R A -  
901 CGGGGCTTCGGCCTGCCAGCTGTGGACCCCAAGAACTAGACAGAACTCATGCCAGT 960  
-----+-----+-----+-----+-----+-----+  
GCCCCGAAGCCGGACGGTCGACACCTGGGGTGTCTTGATCTGTCTTTGAGTACGGTCA  
G L R P A S C G P H K E L D R N S C Q C -  
961 GTGTCTGTAAAACAACACTCTTCCCCAGCCCAATGTGGGCCCAACCGAGAAATTGATGAA 1020  
-----+-----+-----+-----+-----+-----+  
CACAGACATTTTGTGAGAGGGGTCGGTTACACCCCGGTGGCTCTTAAACTACTTT

FIG. 1C

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V C K N K L F P S Q C G A N R E F D E N -  
ACACATGCCAGTGTATGTAAAGAACCTGCCCCAGAAATCAACCCCTAAATCCTGGAA 1080  
-----+-----+-----+-----+-----+-----+-----+  
TGTGTACGGTCACACATACATTTCTTGGACGGGCTCTTAGTTGGGGATTAGGACCTT  
T C C Q C V C K R T C P R N Q P L N P G K -  
AATGTGCCCTGTGAATGTACAGAAAGTCCACAGAAATGCTTGTTAAAGGAAGAGTTCC 1140  
-----+-----+-----+-----+-----+-----+-----+  
TTACACGGACACTTACATGTCTTTTCAGGTGCTTTACGAACAATTTTCCCTTCTCAAGG  
C A C E C T E S P Q K C L L K G K K F H -  
ACCACCAACATGCAGCTGTTACAGACGGCCCATGTACGAACCGCCAGAAAGGCTTGTGAGC 1200  
-----+-----+-----+-----+-----+-----+-----+  
TGGTGGTTTGTACGTCGACAAATGTCTGCCGGTACATGCTTGGCGGTCTTCCGAACACTCG  
H Q T C S C Y R R P C T N R Q K A C E P -  
CAGGATTTTCATATAGTGAAGAAGTGTGTCGTTGTGTCCTTCATATTTGGCAAAGACCAC 1260  
-----+-----+-----+-----+-----+-----+-----+  
GTCCATAAAGTATACACTTCTTCACACAGCAACACAGGAGTATAACCGTTTCTGGTG  
G F S Y S E E V C R C V P S Y W Q R P Q -  
AAATGAGCTAAGATTGTACTGTTTCCAGTTCATCGATTTTCTATTATGGAAACTGTGT

FIG. 1D



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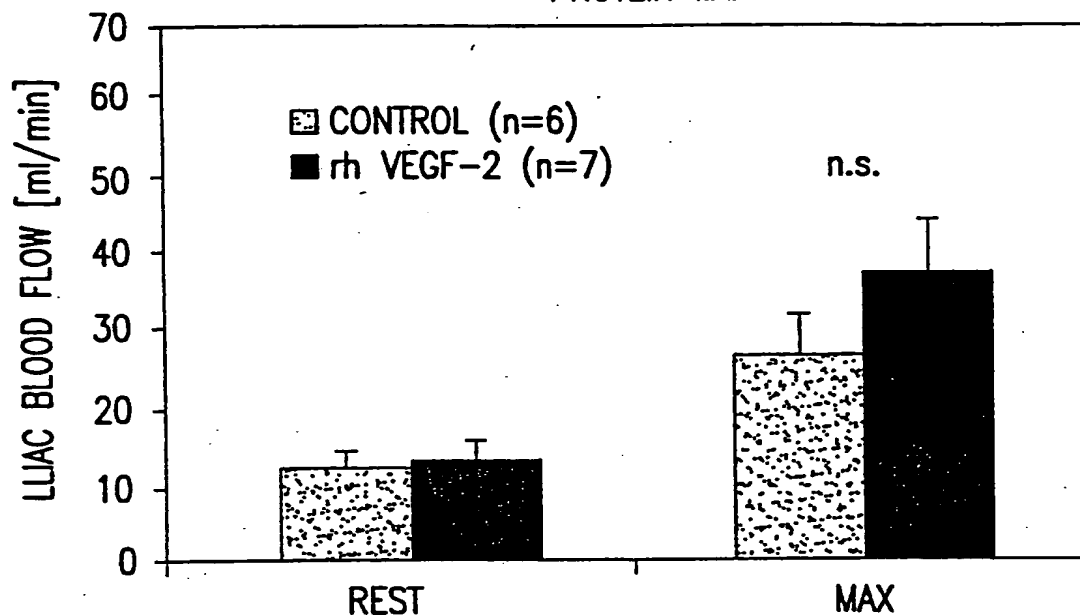
ILIAC BLOOD FLOW  
-PROTEIN I.A.-

FIG.25D

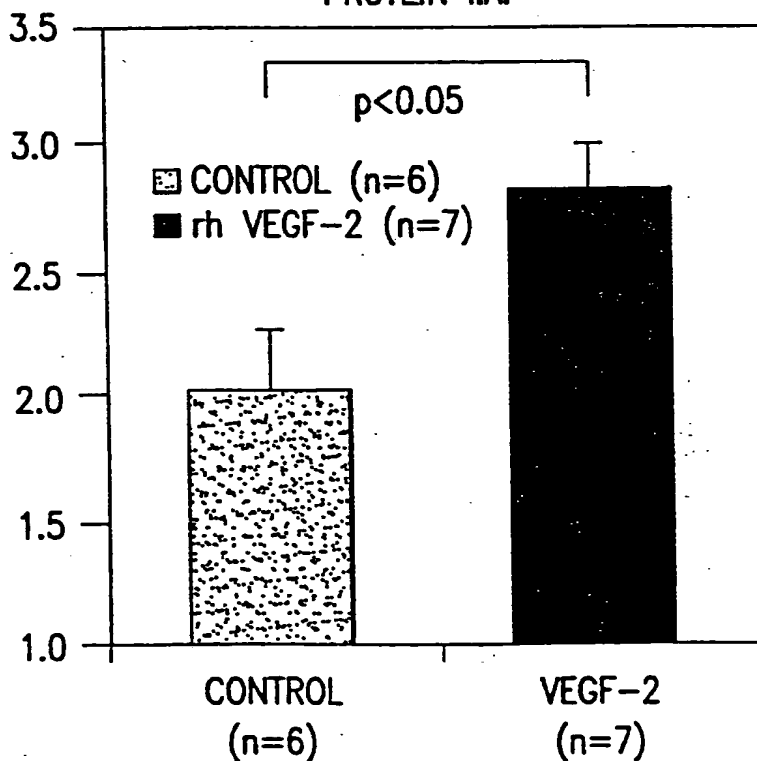
ILIAC FLOW RESERVE  
-PROTEIN I.A.-

FIG.25E

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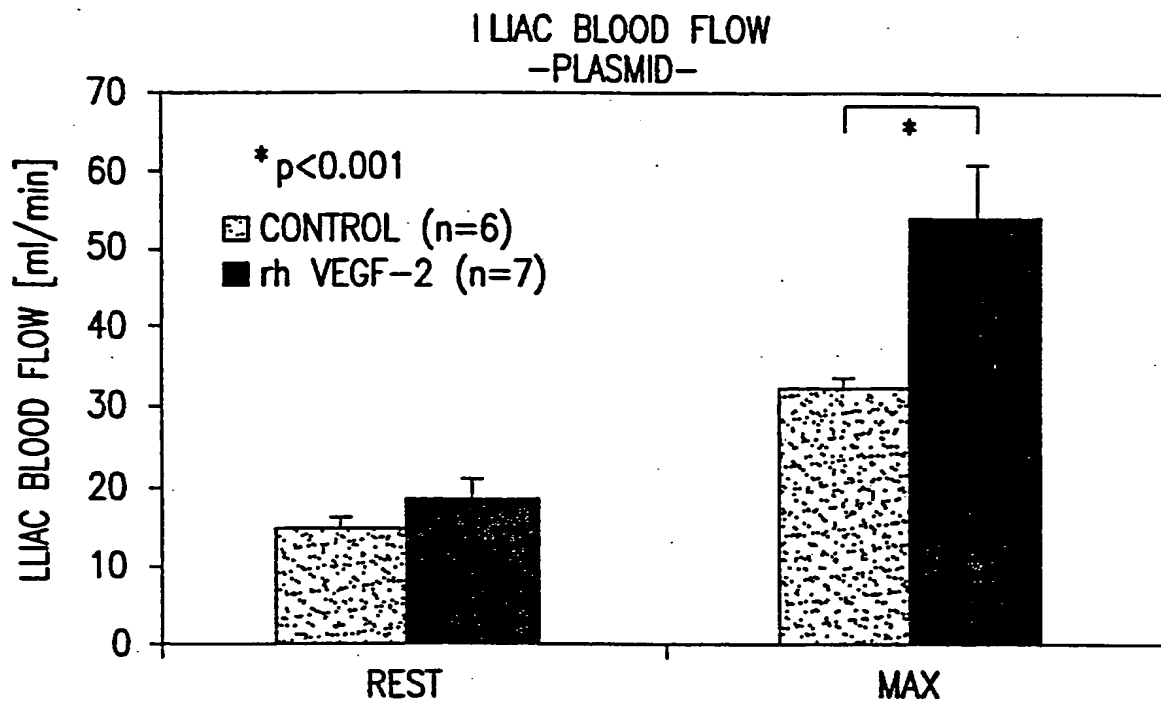


FIG.25F

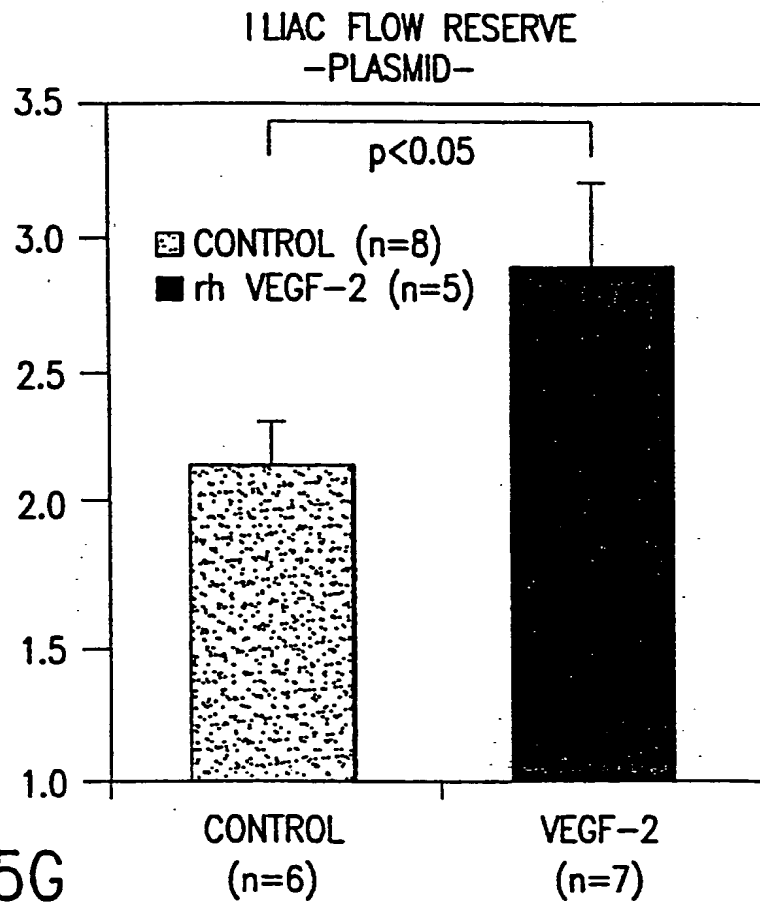


FIG.25G



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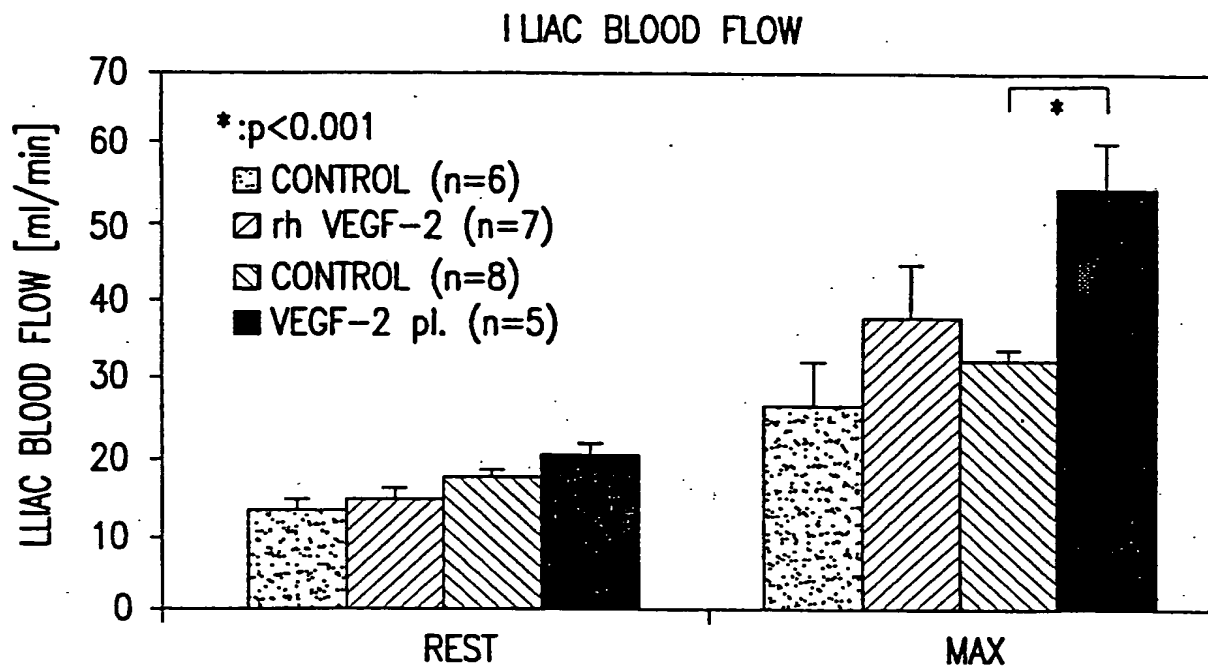


FIG.25H

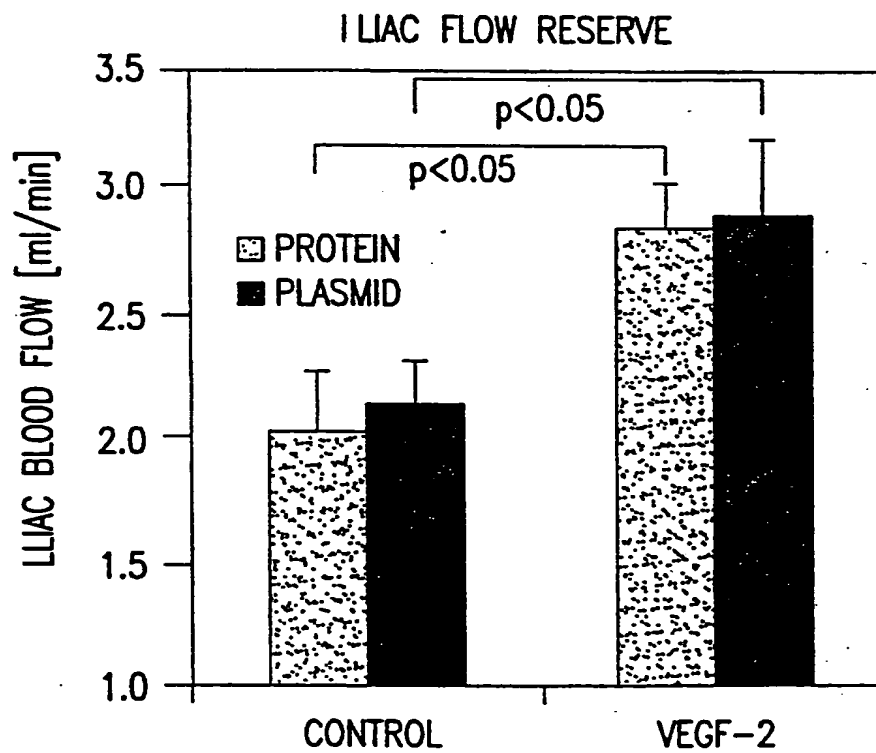


FIG.25I